VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Claims:

Claim 16 has been cancelled.

New claims 22-24 have been added.

Claims 1-15 and 17-21 have been amended as follows:

1. (Amended) A method of removing a part of a transgene after its integration into a genome comprising flanking said part of the transgene on each side thereof with an attachment P region (attP) of bacteriophage λ, wherein the attP region comprises a nucleic acid sequence as set forth in SEQ ID NO:1 or a fragment thereof which maintains the same function, or nucleic acids which hybridise under stringent conditions to the DNA of SEQ ID NO:1 and function as an attP region, or nucleic acids which differ from the DNA of SEQ ID NO:1 due to the degeneracy of the genetic code and which function as an attP region, and inducing a high frequency of intrachromasomal homologous recombination between flanking attP regions, whereby said part of the transgene sandwiched therebetween is removed.

2. (Amended) [A] The method [as claimed in] of Claim 1 [characterised in that] wherein said transgene comprises at least one member selected from the group consisting of a marker gene, a [and/or] vector sequence, and [and/or] other foreign ancillary nucleic acid.

3. (Amended) [A] The method [as claimed in] of Claim 1 [or Claim 2 characterised in that] wherein the marker gene confers resistance to antibiotics [and/or] or herbicide resistance.

4. (Amended) [A] The method [as claimed in any one of the preceding claims characterised in that] of Claim 1 wherein the marker gene is involved in specific biosynthetic pathways [and/or involved in] or environmental tolerance.

5. (Amended) [A] The method [as claimed in any one of the preceding claims characterised in that] of Claim 1 wherein the marker gene is selected from the group consisting of nptII, Ble, dhfr, cat, aphIV, SPT, aaaC3, aaaC4, bar, EPSP, bxn, psbA, tfdA, DHPS, AK, sul, crs1-1 and tdc.

6. (Amended) [A] The method [as claimed in any one of the preceding claims characterised in that] of Claim 1 wherein more than one marker gene, [and/or] vector sequence [and/or] or foreign nucleic acid part is removed from the transgene and each such part [is] to be removed is flanked by an attP region.

7. (Amended) [A] The method [as claimed in any one of the preceding claims characterised in that] of Claim 1 wherein the attP region comprises 352 basepairs, or functionally equivalent fragment thereof, located between positions 27492 and 27844 of bacteriophage λ.

8. (Amended) [A] The method [as claimed in any one of the preceding claims characterised in that] of Claim 1 wherein the attP regions are in a cassette.

9. (Amended) [A] The method [as claimed in] of Claim 8 [characterised in that] wherein the cassette further includes a transformation booster sequence or fragment thereof for enhancing homologous and illegitimate recombination.

10. (Amended) [A] The method [as claimed in] of Claim 8 [or Claim 9 characterised in that] wherein the cassette includes an effector gene such as oryzacyctastin-I or functional equivalent thereof.

11. (Amended) [A] The method [as claimed in any one of the preceding claims characterised in that] of Claim 1 wherein the genome is a plant genome.

12. (Amended) A plant, [or] plant cell or plant tissue [whenever] produced by the method of [any one of Claims 1 to 11] Claim 1.

13. (Amended) A method [which comprises performing the method of Claim 11 to produce a plant or providing a plant or plant cell or plant tissue of Claim 12 and, in either case] of producing a plant comprising the steps:

removing a part of a transgene after its integration into a plant genome comprising flanking said part of the transgene on each side thereof with an attachment P region (attP) of bacteriophage λ, wherein the attP region comprises a nucleic acid sequence as set forth in SEQ ID NO:1 or a fragment thereof which maintains the same function, or nucleic acids which hybridise under stringent conditions to the DNA of SEQ ID NO:1 and function as an attP region, or nucleic acids which differ from the DNA of SEQ ID NO:1 due to the degeneracy of the genetic code and which function as an attP region;

inducing a high frequency of intrachromasomal homologous recombination between flanking attP regions, whereby said part of the transgene sandwiched therebetween is removed; and

growing the plant [and/or harvesting products therefrom].

14. (Amended) A plant, [or] plant cell or plant tissue comprising recombinant attP regions.

15. (Amended) An attP recombination cassette comprising at least one member selected from the group consisting of a marker gene, a [and/or] vector sequence, and [and/or] foreign ancillary nucleic acid flanked on either side by an attP region, wherein the attP region [comprising] comprises a nucleic acid sequence as set forth in SEQ ID NO:1 or a fragment thereof which maintains the same function, or nucleic acids which hybridise under stringent conditions to the DNA of SEQ ID NO:1 and function as an attP region, or nucleic acids which differ from the DNA of SEQ ID NO:1 due to the degeneracy of the genetic code and which function as an attP region.

17. (Amended) A kit for removing a part of a transgene after its integration into a plant genome comprising [an] the attP recombination cassette of [as claimed in] Claim 15.

18. (Amended) A plant, [or] plant cell or plant tissue comprising a recombinant transgene integrated into its genome, wherein [characterised in that] the transgene is associated with a bacteriophage λ attP region on respective sides thereof, wherein the attP region [comprising] comprises a nucleic acid sequence as set forth in SEQ ID NO:1 or a fragment thereof which maintains the same function, or nucleic acids which hybridise under stringent conditions to the DNA of SEQ ID NO:1 and function as an attP region, or nucleic acids which differ from the DNA of SEQ ID NO:1 due to the degeneracy of the genetic code and which function as an attP region.

19. (Amended) [A] The plant, [or] plant cell or plant tissue [as claimed in] of Claim 18 wherein the plant, plant cell or plant tissue comprises [characterised in that it includes] one [such] bacteriophage λ attP region and one effector transgene integrated into its genome.

20. (Amended) [A] The plant, [or] plant cell or plant tissue [as claimed in] of Claim 19 [characterised in that] wherein the bacteriophage λ attP regions and one transgene are not associated with a marker gene, [and/or] vector sequence [and/or] or other foreign ancillary nucleic acid.

21. (Amended) [A] The plant, [or] plant cell or plant tissue [as claimed in any one of Claims 18 to 20] of Claim 18 wherein [characterised in that] the transgene is further associated with a transformation booster sequence or fragment thereof which is capable of enhancing homologous and illegitimate recombination.